

SEQUENCE LISTING

<110> Baxter, John
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<120> NUCLEAR RECEPTOR LIGANDS AND LIGAND BINDING DOMAINS

<130> UCAL-246/02/1US

<140> Not Yet Available

<141> 2000-08-10

<150> US 08/980,115

<151> 1997-11-26

<150> US 08/764,870

<151> 1996-12-13

<150> US 60/008,606

<151> 1995-12-14

<150> US 60/008,543

<151> 1995-12-13

<150> US 60/008,540

<151> 1995-12-13

<160> 17

<170> PatentIn version 3.0

<210> 1

<211> 410

<212> PRT

<213> Rattus sp.

<220>

<221> DOMAIN

<222> (157)..(410)

<223> minimal ligand binding domain

<220>

<221> DOMAIN

<222> (393)..(405)

<223> activation domain

<400> 1

Met Glu Gln Lys Pro Ser Lys Val Glu Cys Gly Ser Asp Pro Glu Glu
1 5 10 15

Asn Ser Ala Arg Ser Pro Asp Gly Lys Arg Lys Arg Lys Asn Gly Gln
20 25 30

Cys Pro Leu Lys Ser Ser Met Ser Gly Tyr Ile Pro Ser Tyr Leu Asp
35 40 45

Lys Asp Glu Gln Cys Val Val Cys Gly Asp Lys Ala Thr Gly Tyr His
50 55 60

Tyr Arg Cys Ile Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr
65 70 75 80

Ile Gln Lys Asn Leu His Pro Thr Tyr Ser Cys Lys Tyr Asp Ser Cys
85 90 95

Cys Val Ile Asp Lys Ile Thr Arg Asn Gln Cys Gln Leu Cys Arg Phe
100 105 110

Lys Lys Cys Ile Ala Val Gly Met Ala Met Asp Leu Val Leu Asp Asp
115 120 125

Ser Lys Arg Val Ala Lys Arg Lys Leu Ile Glu Gln Asn Arg Glu Arg
130 135 140

Arg Arg Lys Glu Glu Met Ile Arg Ser Leu Gln Gln Arg Pro Glu Pro
145 150 155 160

Thr Pro Glu Glu Trp Asp Leu Ile His Val Ala Thr Glu Ala His Arg
165 170 175

Ser Thr Asn Ala Gln Gly Ser His Trp Lys Gln Arg Arg Lys Phe Leu
180 185 190

Pro Asp Asp Ile Gly Gln Ser Pro Ile Val Ser Met Pro Asp Gly Asp
195 200 205

Lys Val Asp Leu Glu Ala Phe Ser Glu Phe Thr Lys Ile Ile Thr Pro
210 215 220

Ala Ile Thr Arg Val Val Asp Phe Ala Lys Lys Leu Pro Met Phe Ser
225 230 235 240

Glu Leu Pro Cys Glu Asp Gln Ile Ile Leu Lys Gly Cys Cys Met
245 250 255

Glu Ile Met Ser Leu Arg Ala Ala Val Arg Tyr Asp Pro Glu Ser Asp
260 265 270

Thr Leu Thr Leu Ser Gly Glu Met Thr Val Lys Arg Lys Gln Leu Lys
275 280 285

Asn Gly Gly Leu Gly Val Val Ser Asp Ala Ile Phe Glu Leu Gly Lys
290 295 300

Ser Leu Ser Ala Phe Asn Leu Asp Asp Thr Glu Val Ala Leu Leu Gln
305 310 315 320

Ala Val Leu Leu Met Ser Thr Asp Arg Ser Gly Leu Leu Cys Val Asp
325 330 335

Lys Ile Glu Lys Ser Gln Glu Ala Tyr Leu Leu Ala Phe Glu His Tyr
340 345 350

Val Asn His Arg Lys His Asn Ile Pro His Phe Trp Pro Lys Leu Leu
355 360 365

Met Lys Val Thr Asp Leu Arg Met Ile Gly Ala Cys His Ala Ser Arg
370 375 380

Phe Leu His Met Lys Val Glu Cys Pro Thr Glu Leu Phe Pro Pro Leu
385 390 395 400

Phe Leu Glu Val Phe Glu Asp Gln Glu Val
405 410

<210> 2

<211> 410

<212> PRT

<213> Homo sapiens

<220>

<221> DOMAIN

<222> (157)..(410)

<223> minimal ligand binding domain

<400> 2

Met Glu Gln Lys Pro Ser Lys Val Glu Cys Gly Ser Asp Pro Glu Glu
1 5 10 15

Asn Ser Ala Arg Ser Pro Asp Gly Lys Arg Lys Arg Lys Asn Gly Gln
20 25 30

Cys Ser Leu Lys Thr Ser Met Ser Gly Tyr Ile Pro Ser Tyr Leu Asp
35 40 45

Lys Asp Glu Gln Cys Val Val Cys Gly Asp Lys Ala Thr Gly Tyr His
50 55 60

Tyr Arg Cys Ile Thr Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg Thr
65 70 75 80

Ile Gln Lys Asn Leu His Pro Thr Tyr Ser Cys Lys Tyr Asp Ser Cys
85 90 95

Cys Val Ile Asp Lys Ile Thr Arg Asn Gln Cys Gln Leu Cys Arg Phe
100 105 110

Lys Lys Cys Ile Ala Val Gly Met Ala Met Asp Leu Val Leu Asp Asp
115 120 125

Ser Lys Arg Val Ala Lys Arg Lys Leu Ile Glu Gln Asn Arg Glu Arg
130 135 140

Arg Arg Lys Glu Glu Met Ile Arg Ser Leu Gln Gln Arg Pro Glu Pro
145 150 155 160

0
1
2
3
4
5
6
7
8
9

Thr Pro Glu Glu Trp Asp Leu Ile His Ile Ala Thr Glu Ala His Arg
165 170 175

Ser Thr Asn Ala Gln Gly Ser His Trp Lys Gln Arg Arg Lys Phe Leu
180 185 190

Pro Asp Asp Ile Gly Gln Ser Pro Ile Val Ser Met Pro Asp Gly Asp
195 200 205

Lys Val Asp Leu Glu Ala Phe Ser Glu Phe Thr Lys Ile Ile Thr Pro
210 215 220

Ala Ile Thr Arg Val Val Asp Phe Ala Lys Lys Leu Pro Met Phe Ser
225 230 235 240

Glu Leu Pro Cys Glu Asp Gln Ile Ile Leu Leu Lys Gly Cys Cys Met
245 250 255

Glu Ile Met Ser Leu Arg Ala Ala Val Arg Tyr Asp Pro Glu Ser Asp
260 265 270

Thr Leu Thr Leu Ser Gly Glu Met Ala Val Lys Arg Glu Gln Leu Lys
275 280 285

Asn Gly Gly Leu Gly Val Val Ser Asp Ala Ile Phe Glu Leu Gly Lys
290 295 300

Ser Leu Ser Ala Phe Asn Leu Asp Asp Thr Glu Val Ala Leu Leu Gln
305 310 315 320

Ala Val Leu Leu Met Ser Thr Asp Arg Ser Gly Leu Leu Cys Val Asp
325 330 335

Lys Ile Glu Lys Ser Gln Glu Ala Tyr Leu Leu Ala Phe Glu His Tyr
340 345 350

Val Asn His Arg Lys His Asn Ile Pro His Phe Trp Pro Lys Leu Leu
355 360 365

Met Lys Val Thr Asp Leu Arg Met Ile Gly Ala Cys His Ala Ser Arg
370 375 380

Phe Leu His Met Lys Val Glu Cys Pro Thr Glu Leu Phe Pro Pro Leu
385 390 395 400

Phe Leu Glu Val Phe Glu Asp Gln Glu Val
405 410

<210> 3
<211> 461
<212> PRT
<213> Homo sapiens

<220>
<221> DOMAIN
<222> (211)..(461)

<223> minimal ligand binding domain

<400> 3

Met Thr Pro Asn Ser Met Thr Glu Asn Gly Leu Thr Ala Trp Asp Lys
1 5 10 15

Pro Lys His Cys Pro Asp Arg Glu His Asp Trp Lys Leu Val Gly Met
20 25 30

Ser Glu Ala Cys Leu His Arg Lys Ser His Ser Glu Arg Arg Ser Thr
35 40 45

Leu Lys Asn Glu Gln Ser Ser Pro His Leu Ile Gln Thr Thr Trp Thr
50 55 60

Ser Ser Ile Phe His Leu Asp His Asp Asp Val Asn Asp Gln Ser Val
65 70 75 80

Ser Ser Ala Gln Thr Phe Gln Thr Glu Glu Lys Lys Cys Lys Gly Tyr
85 90 95

Ile Pro Ser Tyr Leu Asp Lys Asp Glu Leu Cys Val Val Cys Gly Asp
100 105 110

Lys Ala Thr Gly Tyr His Tyr Arg Cys Ile Thr Cys Glu Gly Cys Lys
115 120 125

Gly Phe Phe Arg Arg Thr Ile Gln Lys Asn Leu His Pro Ser Tyr Ser
130 135 140

Cys Lys Tyr Glu Gly Lys Cys Val Ile Asp Lys Val Thr Arg Asn Gln
145 150 155 160

Cys Gln Glu Cys Arg Phe Lys Lys Cys Ile Tyr Val Gly Met Ala Thr
165 170 175

Asp Leu Val Leu Asp Asp Ser Lys Arg Leu Ala Lys Arg Lys Leu Ile
180 185 190

Glu Glu Asn Arg Glu Lys Arg Arg Glu Glu Leu Gln Lys Ser Ile
195 200 205

Gly His Lys Pro Glu Pro Thr Asp Glu Glu Trp Glu Leu Ile Lys Thr
210 215 220

Val Thr Glu Ala His Val Ala Thr Asn Ala Gln Gly Ser His Trp Lys
225 230 235 240

Gln Lys Pro Lys Phe Leu Pro Glu Asp Ile Gly Gln Ala Pro Ile Val
245 250 255

Asn Ala Pro Glu Gly Gly Lys Val Asp Leu Glu Ala Phe Ser His Phe
260 265 270

Thr Lys Ile Ile Thr Pro Ala Ile Thr Arg Val Val Asp Phe Ala Lys

275

280

285

Lys Leu Pro Met Phe Cys Glu Leu Pro Cys Glu Asp Gln Ile Ile Leu
290 295 300

Leu Lys Gly Cys Cys Met Glu Ile Met Ser Leu Arg Ala Ala Val Arg
305 310 315 320

Tyr Asp Pro Glu Ser Glu Thr Leu Thr Leu Asn Gly Glu Met Ala Val
325 330 335

Ile Arg Gly Gln Leu Lys Asn Gly Gly Leu Gly Val Val Ser Asp Ala
340 345 350

Ile Phe Asp Leu Gly Met Ser Leu Ser Ser Phe Asn Leu Asp Asp Thr
355 360 365

Glu Val Ala Leu Leu Gln Ala Val Leu Leu Met Ser Ser Asp Arg Pro
370 375 380

Gly Leu Ala Cys Val Glu Arg Ile Glu Lys Tyr Gln Asp Ser Phe Leu
385 390 395 400

Leu Ala Phe Glu His Tyr Ile Asn Tyr Arg Lys His His Val Thr His
405 410 415

Phe Trp Pro Lys Leu Leu Met Lys Val Thr Asp Leu Arg Met Ile Gly
420 425 430

Ala Cys His Ala Ser Arg Phe Leu His Met Lys Val Glu Cys Pro Thr
435 440 445

Glu Leu Leu Pro Pro Leu Phe Leu Glu Val Phe Glu Asp
450 455 460

<210> 4

<211> 416

<212> PRT

<213> Homo sapiens

<220>

<221> DOMAIN

<222> (131)..(373)

<223> minimal ligand binding domain

<400> 4

Pro Asn Ser Asn His Val Ala Ser Gly Ala Gly Glu Ala Ala Ile Glu
1 5 10 15

Thr Gln Ser Ser Ser Ser Glu Glu Ile Val Pro Ser Pro Pro Ser Pro
20 25 30

Pro Pro Leu Pro Arg Ile Tyr Lys Pro Cys Phe Val Cys Gln Asp Lys
35 40 45

Ser Ser Gly Tyr His Tyr Gly Val Ser Ala Cys Glu Gly Cys Lys Gly
50 55 60

Phe Phe Arg Arg Ser Ile Gln Lys Asn Met Val Tyr Thr Cys His Arg
65 70 75 80

Asp Lys Asn Cys Ile Ile Asn Lys Val Thr Arg Asn Arg Cys Gln Tyr
85 90 95

Cys Arg Leu Gln Lys Cys Phe Glu Val Gly Met Ser Lys Glu Ser Val
100 105 110

Arg Asn Asp Arg Asn Lys Lys Lys Glu Val Pro Lys Pro Glu Cys
115 120 125

Ser Glu Ser Tyr Thr Leu Thr Pro Glu Val Gly Glu Leu Ile Glu Lys
130 135 140

Val Arg Lys Ala His Gln Glu Thr Phe Pro Ala Leu Cys Gln Leu Gly
145 150 155 160

Lys Tyr Thr Thr Asn Asn Ser Ser Glu Gln Arg Val Ser Leu Asp Ile
165 170 175

Asp Leu Trp Asp Lys Phe Ser Glu Leu Ser Thr Lys Cys Ile Ile Lys
180 185 190

Thr Val Glu Phe Ala Lys Gln Leu Pro Gly Phe Thr Thr Leu Thr Ile
195 200 205

Ala Asp Gln Ile Thr Leu Leu Lys Ala Ala Cys Leu Asp Ile Leu Ile
210 215 220

Leu Arg Ile Cys Thr Arg Tyr Thr Pro Glu Gln Asp Thr Met Thr Phe
225 230 235 240

Ser Asp Gly Leu Thr Leu Asn Arg Thr Gln Met His Asn Ala Gly Phe
245 250 255

Gly Pro Leu Thr Asp Leu Val Phe Ala Phe Ala Asn Gln Leu Leu Pro
260 265 270

Leu Glu Met Asp Asp Ala Glu Thr Gly Ile Leu Ser Ala Ile Cys Leu
275 280 285

Ile Cys Gly Asp Arg Gln Asp Leu Glu Gln Pro Asp Arg Val Asp Met
290 295 300

Leu Gln Glu Pro Leu Leu Glu Ala Leu Lys Val Tyr Val Arg Lys Arg
305 310 315 320

Arg Pro Ser Arg Pro His Met Phe Pro Lys Met Leu Met Lys Ile Thr
325 330 335

Asp Leu Arg Ser Ile Ser Ala Lys Gly Ala Glu Arg Val Ile Thr Leu
340 345 350

Lys Met Glu Ile Pro Gly Ser Met Pro Pro Leu Ile Gln Glu Met Leu
355 360 365

Glu Asn Ser Glu Gly Leu Asp Thr Leu Ser Gly Gln Pro Gly Gly Gly
370 375 380

Gly Arg Asp Gly Gly Leu Ala Pro Pro Gly Ser Cys Ser Pro
385 390 395 400

Ser Leu Ser Pro Ser Ser Asn Arg Ser Ser Pro Ala Thr His Ser Pro
405 410 415

<210> 5

<211> 454

<212> PRT

<213> Homo sapiens

<220>

<221> DOMAIN

<222> (179)..(421)

<223> minimal ligand binding domain

<400> 5

Met Ala Thr Asn Lys Glu Arg Leu Phe Ala Ala Gly Ala Leu Gly Pro
1 5 10 15

Gly Ser Gly Tyr Pro Gly Ala Gly Phe Pro Phe Ala Phe Pro Gly Ala
20 25 30

Leu Arg Gly Ser Pro Pro Phe Glu Met Leu Ser Pro Ser Phe Arg Gly
35 40 45

Leu Gly Gln Pro Asp Leu Pro Lys Glu Met Ala Ser Leu Ser Val Glu
50 55 60

Thr Gln Ser Thr Ser Ser Glu Glu Met Val Pro Ser Ser Pro Ser Pro
65 70 75 80

Pro Pro Pro Pro Arg Val Tyr Lys Pro Cys Phe Val Cys Asn Asp Lys
85 90 95

Ser Ser Gly Tyr His Tyr Gly Val Ser Ser Cys Glu Gly Cys Lys Gly
100 105 110

Phe Phe Arg Arg Ser Ile Gln Lys Asn Met Val Tyr Thr Cys His Arg
115 120 125

Asp Lys Asn Cys Ile Ile Asn Lys Val Thr Arg Asn Arg Cys Gln Tyr
130 135 140

Cys Arg Leu Gln Lys Cys Phe Glu Val Gly Met Ser Lys Glu Ala Val
145 150 155 160

Arg Asn Asp Arg Asn Lys Lys Lys Glu Val Lys Glu Glu Gly Ser
165 170 175

Pro Asp Ser Tyr Glu Leu Ser Pro Gln Leu Glu Glu Leu Ile Thr Lys
180 185 190

Val Ser Lys Ala His Gln Glu Thr Phe Pro Ser Leu Cys Gln Leu Gly
195 200 205

Lys Tyr Thr Thr Asn Ser Ser Ala Asp His Arg Val Gln Leu Asp Leu
210 215 220

Gly Leu Trp Asp Lys Phe Ser Glu Leu Ala Thr Lys Cys Ile Ile Lys
225 230 235 240

Ile Val Glu Phe Ala Lys Arg Leu Pro Gly Phe Thr Gly Leu Ser Ile
245 250 255

Ala Asp Gln Ile Thr Leu Leu Lys Ala Ala Cys Leu Asp Ile Leu Met
260 265 270

Leu Arg Ile Cys Thr Arg Tyr Thr Pro Glu Gln Asp Thr Met Thr Phe
275 280 285

Ser Asp Gly Leu Thr Leu Asn Arg Thr Gln Met His Asn Ala Gly Phe
290 295 300

Gly Pro Leu Thr Asp Leu Val Phe Ala Phe Ala Gly Gln Leu Leu Pro
305 310 315 320

Leu Glu Met Asp Asp Thr Glu Thr Gly Leu Leu Ser Ala Ile Cys Leu
325 330 335

Ile Cys Gly Asp Arg Met Asp Leu Glu Glu Pro Glu Lys Val Asp Lys
340 345 350

Leu Gln Glu Pro Leu Leu Glu Ala Leu Arg Leu Tyr Ala Arg Arg Arg
355 360 365

Arg Pro Ser Gln Pro Tyr Met Phe Pro Arg Met Leu Met Lys Ile Thr
370 375 380

Asp Leu Arg Gly Ile Ser Thr Lys Gly Ala Glu Arg Ala Ile Thr Leu
385 390 395 400

Lys Met Glu Ile Pro Gly Pro Met Pro Pro Leu Ile Arg Glu Met Leu
405 410 415

Glu Asn Pro Glu Met Phe Glu Asp Asp Ser Ser Gln Pro Gly Pro His
420 425 430

Pro Asn Ala Ser Ser Glu Asp Glu Val Pro Gly Gly Gln Gly Lys Gly
435 440 445

Gly Leu Lys Ser Pro Ala
450

<210> 6
<211> 462

<212> PRT
<213> Homo sapiens

<220>
<221> DOMAIN
<222> (231)..(460)
<223> minimal ligand binding domain

<400> 6

Met Asp Thr Lys His Phe Leu Pro Leu Asp Phe Ser Thr Gln Val Asn
1 5 10 15

Ser Ser Leu Thr Ser Pro Thr Gly Arg Gly Ser Met Ala Ala Pro Ser
20 25 30

Leu His Pro Ser Leu Gly Pro Gly Ile Gly Ser Pro Gly Gln Leu His
35 40 45

Ser Pro Ile Ser Thr Leu Ser Ser Pro Ile Asn Gly Met Gly Pro Pro
50 55 60

Phe Ser Val Ile Ser Ser Pro Met Gly Pro His Ser Met Ser Val Pro
65 70 75 80

Thr Thr Pro Thr Leu Gly Phe Ser Thr Gly Ser Pro Gln Leu Ser Ser
85 90 95

Pro Met Asn Pro Val Ser Ser Ser Glu Asp Ile Lys Pro Pro Leu Gly
100 105 110

Leu Asn Gly Val Leu Lys Val Pro Ala His Pro Ser Gly Asn Met Ala
115 120 125

Ser Phe Thr Lys His Ile Cys Ala Ile Cys Gly Asp Arg Ser Ser Gly
130 135 140

Lys His Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys
145 150 155 160

Arg Thr Val Arg Lys Asp Leu Thr Tyr Thr Cys Arg Asp Asn Lys Asp
165 170 175

Cys Leu Ile Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr Cys Arg Tyr
180 185 190

Gln Lys Cys Leu Ala Met Gly Met Lys Arg Glu Ala Val Gln Glu Glu
195 200 205

Arg Gln Arg Gly Lys Asp Arg Asn Glu Asn Glu Val Glu Ser Thr Ser
210 215 220

Ser Ala Asn Glu Asp Met Pro Val Glu Arg Ile Leu Glu Ala Glu Leu
225 230 235 240

Ala Val Glu Pro Lys Thr Glu Thr Tyr Val Glu Ala Asn Met Gly Leu

DRAFT DATE 2010

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245 250 255

Asn Pro Ser Ser Pro Asn Asp Pro Val Thr Asn Ile Cys Gln Ala Ala
260 265 270

Asp Lys Gln Leu Phe Thr Leu Val Glu Trp Ala Lys Arg Ile Pro His
275 280 285

Phe Ser Glu Leu Pro Leu Asp Asp Gln Val Ile Leu Leu Arg Ala Gly
290 295 300

Trp Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser Ile Ala Val
305 310 315 320

Lys Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val His Arg Asn Ser
325 330 335

Ala His Ser Ala Gly Val Gly Ala Ile Phe Asp Arg Val Leu Thr Glu
340 345 350

Leu Val Ser Lys Met Arg Asp Met Gln Met Asp Lys Thr Glu Leu Gly
355 360 365

Cys Leu Arg Ala Ile Val Leu Phe Asn Pro Asp Ser Lys Gly Leu Ser
370 375 380

Asn Pro Ala Glu Val Glu Ala Leu Arg Glu Lys Val Tyr Ala Ser Leu
385 390 395 400

Glu Ala Tyr Cys Lys His Lys Tyr Pro Glu Gln Pro Gly Arg Phe Ala
405 410 415

Lys Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly Leu Lys Cys
420 425 430

Leu Glu His Leu Phe Phe Lys Leu Ile Gly Asp Thr Pro Ile Asp
435 440 445

Thr Phe Leu Met Glu Met Leu Glu Ala Pro His Gln Met Thr
450 455 460

<210> 7

<211> 525

<212> PRT

<213> Homo sapiens

<220>

<221> DOMAIN

<222> (292)..(523)

<223> minimal ligand binding domain

<400> 7

Met Ser Trp Ala Ala Arg Pro Pro Phe Leu Pro Gln Arg His Ala Glu
1 5 10 15

DRAFT

Gly Ser Val Gly Arg Trp Gly Ala Lys Glu Cys Ile Val Gly Ser Ala
20 25 30

Thr Ala Leu Ala Gly Ser Arg Ser Gly Gly Gly Gly Gly Arg
35 40 45

Arg Arg Thr Thr Asn Pro Gly Ala Gly Ala Arg Gly Trp Thr Gly Arg
50 55 60

Asp Gly Arg His Gly Arg Asp Ser Arg Ser Pro Asp Ser Ser Ser Pro
65 70 75 80

Asn Pro Leu Pro Gln Gly Val Pro Pro Pro Ser Pro Pro Gly Pro Pro
85 90 95

Leu Pro Pro Ser Thr Ala Pro Thr Leu Gly Gly Ser Gly Ala Pro Pro
100 105 110

Pro Pro Pro Met Pro Pro Pro Pro Leu Gly Ser Pro Phe Pro Val Ile
115 120 125

Ser Ser Ser Met Gly Ser Pro Gly Leu Pro Pro Pro Ala Pro Pro Gly
130 135 140

Phe Ser Gly Pro Val Ser Ser Pro Gln Ile Asn Ser Thr Val Ser Leu
145 150 155 160

Pro Gly Gly Ser Gly Pro Pro Glu Asp Val Lys Pro Pro Val Leu
165 170 175

Gly Val Arg Gly Leu His Cys Pro Pro Pro Gly Gly Pro Gly Ala
180 185 190

Gly Lys Arg Leu Cys Ala Ile Cys Gly Asp Arg Ser Ser Gly Lys His
195 200 205

Tyr Gly Val Tyr Ser Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr
210 215 220

Ile Arg Lys Asp Leu Thr Tyr Ser Cys Arg Asp Asn Lys Asp Cys Thr
225 230 235 240

Val Asp Lys Arg Gln Arg Asn Arg Cys Gln Tyr Cys Arg Tyr Gln Lys
245 250 255

Cys Leu Ala Thr Gly Met Lys Arg Glu Ala Val Gln Glu Arg Gln
260 265 270

Arg Gly Lys Asp Lys Asp Gly Asp Gly Glu Cys Ala Gly Gly Ala Pro
275 280 285

Glu Glu Met Pro Val Asp Arg Ile Leu Glu Ala Glu Leu Ala Val Glu
290 295 300

Gln Lys Ser Asp Gln Gly Val Glu Gly Pro Gly Gly Thr Gly Gly Ser
305 310 315 320

Gly Ser Ser Pro Asn Asp Pro Val Thr Asn Ile Cys Gln Ala Ala Asp
325 330 335

Lys Gln Leu Phe Thr Leu Val Glu Trp Ala Lys Arg Ile Pro His Phe
340 345 350

Ser Ser Leu Pro Leu Asp Asp Gln Val Ile Leu Leu Arg Ala Gly Trp
355 360 365

Asn Glu Leu Leu Ile Ala Ser Phe Ser His Arg Ser Ile Asp Val Arg
370 375 380

Asp Gly Ile Leu Leu Ala Thr Gly Leu His Val His Arg Asn Ser Ala
385 390 395 400

His Ser Ala Gly Val Gly Ala Ile Phe Asp Arg Val Leu Thr Glu Leu
405 410 415

Val Ser Lys Met Arg Asp Met Arg Met Asp Lys Thr Glu Leu Gly Cys
420 425 430

Leu Arg Ala Ile Ile Leu Phe Asn Pro Asp Ala Lys Gly Leu Ser Asn
435 440 445

Pro Ser Glu Val Glu Val Leu Arg Glu Lys Val Tyr Ala Ser Leu Glu
450 455 460

Thr Tyr Cys Lys Gln Lys Tyr Pro Glu Gln Gln Gly Arg Phe Ala Lys
465 470 475 480

Leu Leu Leu Arg Leu Pro Ala Leu Arg Ser Ile Gly Leu Lys Cys Leu
485 490 495

Glu His Leu Phe Phe Lys Leu Ile Gly Asp Thr Pro Ile Asp Thr
500 505 510

Phe Leu Met Glu Met Leu Glu Ala Pro His Gln Leu Ala
515 520 525

<210> 8
<211> 468
<212> PRT
<213> Homo sapiens

<220>
<221> DOMAIN
<222> (196)..(468)
<223> minimal ligand binding domain

<400> 8

Met Val Asp Thr Glu Ser Pro Leu Cys Pro Leu Ser Pro Leu Glu Ala
1 5 10 15

Gly Asp Leu Glu Ser Pro Leu Ser Glu Glu Phe Leu Gln Glu Met Gly
20 25 30

Asn Ile Gln Glu Ile Ser Gln Ser Ile Gly Glu Asp Ser Ser Gly Ser
35 40 45

Phe Gly Phe Thr Glu Tyr Gln Tyr Leu Gly Ser Cys Pro Gly Ser Asp
50 55 60

Gly Ser Val Ile Thr Asp Thr Leu Ser Pro Ala Ser Ser Pro Ser Ser
65 70 75 80

Val Thr Tyr Pro Val Val Pro Gly Ser Val Asp Glu Ser Pro Ser Gly
85 90 95

Ala Leu Asn Ile Glu Cys Arg Ile Cys Gly Asp Lys Ala Ser Gly Tyr
100 105 110

His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly Phe Phe Arg Arg
115 120 125

Thr Ile Arg Leu Lys Leu Val Tyr Asp Lys Cys Asp Arg Ser Cys Lys
130 135 140

Ile Gln Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys Arg Phe His Lys
145 150 155 160

Cys Leu Ser Val Gly Met Ser His Asn Ala Ile Arg Phe Gly Arg Met
165 170 175

Pro Arg Ser Glu Lys Ala Lys Leu Lys Ala Glu Ile Leu Thr Cys Glu
180 185 190

His Asp Ile Glu Asp Ser Glu Thr Ala Asp Leu Lys Ser Leu Ala Lys
195 200 205

Arg Ile Tyr Glu Ala Tyr Leu Lys Asn Phe Asn Met Asn Lys Val Lys
210 215 220

Ala Arg Val Ile Leu Ser Gly Lys Ala Ser Asn Asn Pro Pro Phe Val
225 230 235 240

Ile His Asp Met Glu Thr Leu Cys Met Ala Glu Lys Thr Leu Val Ala
245 250 255

Lys Leu Val Ala Asn Gly Ile Gln Asn Lys Glu Val Glu Val Arg Ile
260 265 270

Phe His Cys Cys Gln Cys Thr Ser Val Glu Thr Val Thr Glu Leu Thr
275 280 285

Glu Phe Ala Lys Ala Ile Pro Ala Phe Ala Asn Leu Asp Leu Asn Asp
290 295 300

Gln Val Thr Leu Leu Lys Tyr Gly Val Tyr Glu Ala Ile Phe Ala Met
305 310 315 320

Leu Ser Ser Val Met Asn Lys Asp Gly Met Leu Val Ala Tyr Gly Asn
325 330 335

Q Q Q T P D E F A G S D E R C

Gly Phe Ile Thr Arg Glu Phe Leu Lys Ser Leu Arg Lys Pro Phe Cys
340 345 350

Asp Ile Met Glu Pro Lys Phe Asp Phe Ala Met Lys Phe Asn Ala Leu
355 360 365

Glu Leu Asp Asp Ser Asp Ile Ser Leu Phe Val Ala Ala Ile Ile Cys
370 375 380

Cys Gly Asp Arg Pro Gly Leu Leu Asn Val Gly His Ile Glu Lys Met
385 390 395 400

Gln Glu Gly Ile Val His Val Leu Arg Leu His Leu Gln Ser Asn His
405 410 415

Pro Asp Asp Ile Phe Leu Phe Pro Lys Leu Leu Gln Lys Met Ala Asp
420 425 430

Leu Arg Gln Leu Val Thr Glu His Ala Gln Leu Val Gln Ile Ile Lys
435 440 445

Lys Thr Glu Ser Asp Ala Ala Leu His Pro Leu Leu Gln Glu Ile Tyr
450 455 460

Arg Asp Met Tyr
465

<210> 9
<211> 441
<212> PRT
<213> Homo sapiens

<220>
<221> DOMAIN
<222> (168)..(441)
<223> minimal ligand binding domain

<400> 9

Met Glu Gln Pro Gln Glu Glu Ala Pro Glu Val Arg Glu Glu Glu
1 5 10 15

Lys Glu Glu Val Ala Glu Ala Glu Gly Ala Pro Glu Leu Asn Gly Gly
20 25 30

Pro Gln His Ala Leu Pro Ser Ser Ser Tyr Thr Asp Leu Ser Arg Ser
35 40 45

Ser Ser Pro Pro Ser Leu Leu Asp Gln Leu Gln Met Gly Cys Asp Gly
50 55 60

Ala Ser Cys Gly Ser Leu Asn Met Glu Cys Arg Val Cys Gly Asp Lys
65 70 75 80

Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly Cys Lys Gly

| 85 | 90 | 95 | |
|---|-----|-----|-----|
| Phe Phe Arg Arg Thr Ile Arg Met Lys Leu Glu Tyr Glu Lys Cys Glu | | | |
| 100 | 105 | 110 | |
| Arg Ser Cys Lys Ile Gln Lys Lys Asn Arg Asn Lys Cys Gln Tyr Cys | | | |
| 115 | 120 | 125 | |
| Arg Phe Gln Lys Cys Leu Ala Leu Gly Met Ser His Asn Ala Ile Arg | | | |
| 130 | 135 | 140 | |
| Phe Gly Arg Met Pro Glu Ala Glu Lys Arg Lys Leu Val Ala Gly Leu | | | |
| 145 | 150 | 155 | 160 |
| Thr Ala Asn Glu Gly Ser Gln Tyr Asn Pro Gln Val Ala Asp Leu Lys | | | |
| 165 | 170 | 175 | |
| Ala Phe Ser Lys His Ile Tyr Asn Ala Tyr Leu Lys Asn Phe Asn Met | | | |
| 180 | 185 | 190 | |
| Thr Lys Lys Ala Arg Ser Ile Leu Thr Gly Lys Ala Ser His Thr | | | |
| 195 | 200 | 205 | |
| Ala Pro Phe Val Ile His Asp Ile Glu Thr Leu Trp Gln Ala Glu Lys | | | |
| 210 | 215 | 220 | |
| Gly Leu Val Trp Lys Gln Leu Val Asn Gly Leu Pro Pro Tyr Lys Glu | | | |
| 225 | 230 | 235 | 240 |
| Ile Ser Val His Val Phe Tyr Arg Cys Gln Cys Thr Thr Val Glu Thr | | | |
| 245 | 250 | 255 | |
| Val Arg Glu Leu Thr Glu Phe Ala Lys Ser Ile Pro Ser Phe Ser Ser | | | |
| 260 | 265 | 270 | |
| Leu Phe Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val His Glu | | | |
| 275 | 280 | 285 | |
| Ala Ile Phe Ala Met Leu Ala Ser Ile Val Asn Lys Asp Gly Leu Leu | | | |
| 290 | 295 | 300 | |
| Val Ala Asn Gly Ser Gly Phe Val Thr Arg Glu Phe Leu Arg Ser Leu | | | |
| 305 | 310 | 315 | 320 |
| Arg Lys Pro Phe Ser Asp Ile Ile Glu Pro Lys Phe Glu Phe Ala Val | | | |
| 325 | 330 | 335 | |
| Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Leu Phe Ile | | | |
| 340 | 345 | 350 | |
| Ala Ala Ile Ile Leu Cys Gly Asp Arg Pro Gly Leu Met Asn Val Pro | | | |
| 355 | 360 | 365 | |
| Arg Val Glu Ala Ile Gln Asp Thr Ile Leu Arg Ala Leu Glu Phe His | | | |
| 370 | 375 | 380 | |
| Leu Gln Ala Asn His Pro Asp Ala Gln Tyr Leu Phe Pro Lys Leu Leu | | | |

385 390 395 400

Gln Lys Met Ala Asp Leu Arg Gln Leu Val Thr Glu His Ala Gln Met
405 410 415

Met Gln Arg Ile Lys Lys Thr Glu Thr Ser Leu His Pro Leu
420 425 430

Leu Gln Glu Ile Tyr Lys Asp Met Tyr
435 440

<210> 10

<211> 475

<212> PRT

<213> Homo sapiens

<220>

<221> DOMAIN

<222> (202)..(475)

<223> minimal ligand binding domain

<400> 10

Met Val Asp Thr Glu Met Pro Phe Trp Pro Thr Asn Phe Gly Ile Ser
1 5 10 15

Ser Val Asp Leu Ser Met Met Asp Asp His Ser His Ser Phe Asp Ile
20 25 30

Lys Pro Phe Thr Thr Val Asp Phe Ser Ser Ile Ser Ala Pro His Tyr
35 40 45

Glu Asp Ile Pro Phe Thr Arg Ala Asp Pro Met Val Ala Asp Tyr Lys
50 55 60

Tyr Asp Leu Lys Leu Gln Glu Tyr Gln Ser Ala Ile Lys Val Glu Pro
65 70 75 80

Ala Ser Pro Pro Tyr Tyr Ser Glu Lys Ala Gln Leu Tyr Asn Arg Pro
85 90 95

His Glu Glu Pro Ser Asn Ser Leu Met Ala Ile Glu Cys Arg Val Cys
100 105 110

Gly Asp Lys Ala Ser Gly Phe His Tyr Gly Val His Ala Cys Glu Gly
115 120 125

Cys Lys Gly Phe Phe Arg Arg Thr Ile Arg Leu Lys Leu Ile Tyr Asp
130 135 140

Arg Cys Asp Leu Asn Cys Arg Ile His Lys Lys Ser Arg Asn Lys Cys
145 150 155 160

Gln Tyr Cys Arg Phe Gln Lys Cys Leu Ala Val Gly Met Ser His Asn
165 170 175

Ala Ile Arg Phe Gly Arg Met Pro Gln Ala Glu Lys Glu Lys Leu Leu
180 185 190

Ala Glu Ile Ser Ser Asp Ile Asp Gln Leu Asn Pro Glu Ser Ala Asp
195 200 205

Leu Arg Ala Leu Ala Lys His Leu Tyr Asp Ser Tyr Ile Lys Ser Phe
210 215 220

Pro Leu Thr Lys Ala Lys Ala Arg Ala Ile Leu Thr Gly Lys Thr Thr
225 230 235 240

Asp Lys Ser Pro Phe Val Ile Tyr Asp Met Asn Ser Leu Met Met Gly
245 250 255

Glu Asp Lys Ile Lys Phe Lys His Ile Thr Pro Leu Gln Glu Gln Ser
260 265 270

Lys Glu Val Ala Ile Arg Ile Phe Gln Gly Cys Gln Phe Arg Ser Val
275 280 285

Glu Ala Val Gln Glu Ile Thr Glu Tyr Ala Lys Asn Ile Pro Gly Phe
290 295 300

Ile Asn Leu Asp Leu Asn Asp Gln Val Thr Leu Leu Lys Tyr Gly Val
305 310 315 320

His Glu Ile Ile Tyr Thr Met Leu Ala Ser Leu Met Asn Lys Asp Gly
325 330 335

Val Leu Ile Ser Glu Gly Gln Gly Phe Met Thr Arg Glu Phe Leu Lys
340 345 350

Ser Leu Arg Lys Pro Phe Gly Asp Phe Met Glu Pro Lys Phe Glu Phe
355 360 365

Ala Val Lys Phe Asn Ala Leu Glu Leu Asp Asp Ser Asp Leu Ala Ile
370 375 380

Phe Ile Ala Val Ile Ile Leu Ser Gly Asp Arg Pro Gly Leu Leu Asn
385 390 395 400

Val Lys Pro Ile Glu Asp Ile Gln Asp Asn Leu Leu Gln Ala Leu Glu
405 410 415

Leu Gln Leu Lys Leu Asn His Pro Glu Ser Ser Gln Leu Phe Ala Lys
420 425 430

Val Leu Gln Lys Met Thr Asp Leu Arg Gln Ile Val Thr Glu His Val
435 440 445

Gln Leu Leu His Val Ile Lys Lys Thr Glu Thr Asp Met Ser Leu His
450 455 460

Pro Leu Leu Gln Glu Ile Tyr Lys Asp Leu Tyr
465 470 475

<210> 11
<211> 609
<212> PRT
<213> Homo sapiens

<220>
<221> DOMAIN
<222> (295)..(585)
<223> minimal ligand binding domain

<400> 11

Met Asp Thr Glu Asp Leu Pro Ala Asn Asn Ala Pro Leu Thr Val Asn
1 5 10 15

Glu Gln Leu Leu Gly Ser Cys Thr Leu Lys Phe Pro Ala Gln Asp Ala
20 25 30

Gln Val Ile Val Met Ser Gly Gln Glu Thr Ile Arg Val Leu Glu Val
35 40 45

Glu Val Asp Thr Ala Leu Ser Ser Ala Gly Ala Ala Glu Ser Gly Gly
50 55 60

Asp Glu Glu Gly Ser Gly Gln Ser Leu Glu Ala Thr Glu Glu Ala Gln
65 70 75 80

Leu Asp Gly Pro Val Thr Thr Ser Ser Thr Thr Ala Val Thr Val Glu
85 90 95

Val Ser Ala Pro Val Val Gln Thr Val Val Ser Lys Ala Ala Ile Ser
100 105 110

Val Ser Pro Ala Gln Gln Thr Ser Val Pro Ile Thr Val Gln Ala Cys
115 120 125

Pro Gln Val Leu Thr Gln Asp Gly Leu Ala Ser Leu Met Thr Gly Met
130 135 140

Leu Ala Gln Gln Ser Ser Leu Gly Gln Pro Leu Leu Ile Pro Leu Ser
145 150 155 160

Met Ala Gly Ser Val Gly Gly Gln Gly Gly Leu Ala Val Leu Thr Leu
165 170 175

Pro Thr Ala Thr Val Ala Thr Leu Pro Gly Leu Ala Ala Ser Pro
180 185 190

Ala Gly Gly Leu Leu Lys Leu Pro Phe Ala Gly Leu Gln Ala Ala Thr
195 200 205

Val Leu Asn Ser Val Gln Thr Gln Leu Gln Ala Pro Ala Gln Ala Val
210 215 220

Leu Gln Pro Gln Met Ser Ala Leu Ala Met Gln Gln Thr Gln Thr Thr
225 230 235 240

Ala Ala Thr Thr Ala Ser Ile Val Gln Lys Ala Ser Glu Pro Ser Val
245 250 255

Ser Val Ala Thr Leu Gln Thr Ala Gly Leu Ser Ile Asn Pro Ala Ile
260 265 270

Ile Ser Ala Ala Ser Leu Gly Ala Gln Pro Gln Phe Ile Ser Ser Leu
275 280 285

Thr Thr Thr Pro Ile Ile Thr Ser Ala Met Ser Asn Val Ala Gly Leu
290 295 300

Thr Ser Gln Leu Ile Thr Asn Ala Gln Gly Gln Val Ile Gly Thr Leu
305 310 315 320

Pro Leu Leu Val Asn Pro Ala Ser Leu Ala Gly Ala Ala Ala Ser
325 330 335

Ala Leu Pro Ala Gln Gly Leu Gln Val Gln Thr Val Ala Pro Gln Leu
340 345 350

Leu Leu Asn Ser Gln Gly Gln Ile Ile Ala Thr Ile Gly Asn Gly Pro
355 360 365

Thr Ala Ala Ile Pro Ser Thr Ala Ser Val Leu Pro Lys Ala Thr Val
370 375 380

Pro Leu Thr Leu Thr Lys Thr Thr Gln Gly Pro Val Gly Lys Val
385 390 395 400

Ala Pro Ser Lys Val Ile Ile Ala Pro Gln Pro Ser Val Val Lys Pro
405 410 415

Val Thr Ser Leu Thr Ala Ala Gly Val Ile Ala Cys Gly Glu Met Pro
420 425 430

Thr Val Gly Gln Leu Val Asn Lys Pro Ser Ala Val Lys Asp Glu Glu
435 440 445

Ala Ile Asn Leu Glu Glu Ile Arg Glu Phe Ala Lys Asn Phe Lys Ile
450 455 460

Arg Arg Leu Ser Leu Gly Leu Thr Gln Thr Gln Val Gly Gln Ala Leu
465 470 475 480

Thr Ala Thr Glu Gly Pro Ala Tyr Ser Gln Ser Ala Ile Cys Arg Phe
485 490 495

Glu Lys Leu Asp Ile Thr Pro Lys Ser Ala Gln Lys Leu Lys Pro Val
500 505 510

Leu Glu Arg Trp Leu Ala Glu Ala Glu Leu Trp Asn Gln Lys Gly Gln
515 520 525

Gln Asn Leu Met Glu Phe Val Gly Gly Glu Pro Ser Lys Lys Arg Lys
530 535 540

Arg Arg Thr Ser Phe Thr Pro Gln Ala Ile Glu Val Leu Asn Thr Tyr
545 550 555 560

Phe Glu Lys Asn Ser Leu Pro Thr Gly Gln Glu Ile Thr Glu Ile Ala
565 570 575

Lys Glu Leu Asn Tyr Asp Arg Glu Val Val Arg Val Trp Phe Cys Asn
580 585 590

Arg Arg Gln Thr Leu Lys Asn Thr Ser Lys Ile Asn Val Phe Gln Ser
595 600 605

Gln

<210> 12
<211> 595
<212> PRT
<213> Homo sapiens

<220>
<221> DOMAIN
<222> (287)..(549)
<223> minimal ligand binding domain

<400> 12

Met Thr Met Thr Leu His Thr Lys Ala Ser Gly Met Ala Leu Leu His
1 5 10 15

Gln Ile Gln Gly Asn Glu Leu Glu Pro Leu Asn Arg Pro Gln Leu Lys
20 25 30

Ile Pro Leu Glu Arg Pro Leu Gly Glu Val Tyr Leu Asp Ser Ser Lys
35 40 45

Pro Ala Val Tyr Asn Tyr Pro Glu Gly Ala Ala Tyr Glu Phe Asn Ala
50 55 60

Ala Ala Ala Asn Ala Gln Val Tyr Gly Gln Thr Gly Leu Pro Tyr
65 70 75 80

Gly Pro Gly Ser Glu Ala Ala Phe Gly Ser Asn Gly Leu Gly Gly
85 90 95

Phe Pro Pro Leu Asn Ser Val Ser Pro Ser Pro Leu Met Leu Leu His
100 105 110

Pro Pro Pro Gln Leu Ser Pro Phe Leu Gln Pro His Gly Gln Gln Val
115 120 125

Pro Tyr Tyr Leu Glu Asn Glu Pro Ser Gly Tyr Thr Val Arg Glu Ala
130 135 140

Gly Pro Pro Ala Phe Tyr Arg Pro Asn Ser Asp Asn Arg Arg Gln Gly

145 150 155 160
Gly Arg Glu Arg Leu Ala Ser Thr Asn Asp Lys Gly Ser Met Ala Met
165 170 175

Glu Ser Ala Lys Glu Thr Arg Tyr Cys Ala Val Cys Asn Asp Tyr Ala
180 185 190

Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe
195 200 205

Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met Cys Pro Ala Thr
210 215 220

Asn Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys
225 230 235 240

Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys Gly Gly Ile Arg
245 250 255

Lys Asp Arg Arg Gly Gly Arg Met Leu Lys His Lys Arg Gln Arg Asp
260 265 270

Asp Gly Glu Gly Arg Gly Glu Val Gly Ser Ala Gly Asp Met Arg Ala
275 280 285

Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys Asn
290 295 300

Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu Leu
305 310 315 320

Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg Pro
325 330 335

Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp Arg
340 345 350

Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe Val
355 360 365

Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp Leu
370 375 380

Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro Gly
385 390 395 400

Lys Leu Leu Phe Ala Pro Asn Leu Leu Asp Arg Asn Gln Gly Lys
405 410 415

Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser
420 425 430

Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys Leu
435 440 445

Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser Ser

450

455

460

Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu Asp
465 470 475 480

Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu Thr
485 490 495

Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu Ser
500 505 510

His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met
515 520 525

Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu
530 535 540

Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser Val
545 550 555 560

Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser Ser
565 570 575

His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe Pro
580 585 590

Ala Thr Val
595

<210> 13
<211> 777
<212> PRT
<213> Homo sapiens

<220>
<221> DOMAIN
<222> (506)..(762)
<223> minimal ligand binding domain

<400> 13

Met Asp Ser Lys Glu Ser Leu Thr Pro Gly Arg Glu Glu Asn Pro Ser
1 5 10 15

Ser Val Leu Ala Gln Glu Arg Gly Asp Val Met Asp Phe Tyr Lys Thr
20 25 30

Leu Arg Gly Gly Ala Thr Val Lys Val Ser Ala Ser Ser Pro Ser Leu
35 40 45

Ala Val Ala Ser Gln Ser Asp Ser Lys Gln Arg Arg Leu Leu Val Asp
50 55 60

Phe Pro Lys Gly Ser Val Ser Asn Ala Gln Gln Pro Asp Leu Ser Lys
65 70 75 80

Ala Val Ser Leu Ser Met Gly Leu Tyr Met Gly Glu Thr Glu Thr Lys
85 90 95

Val Met Gly Asn Asp Leu Gly Phe Pro Gln Gln Gly Gln Ile Ser Leu
100 105 110

Ser Ser Gly Glu Thr Asp Leu Lys Leu Leu Glu Glu Ser Ile Ala Asn
115 120 125

Leu Asn Arg Ser Thr Ser Val Pro Glu Asn Pro Lys Ser Ser Ala Ser
130 135 140

Thr Ala Val Ser Ala Ala Pro Thr Glu Lys Glu Phe Pro Lys Thr His
145 150 155 160

Ser Asp Val Ser Ser Glu Gln Gln His Leu Lys Gly Gln Thr Gly Thr
165 170 175

Asn Gly Gly Asn Val Lys Leu Tyr Thr Thr Asp Gln Ser Thr Phe Asp
180 185 190

Ile Leu Gln Asp Leu Glu Phe Ser Ser Gly Ser Pro Gly Lys Glu Thr
195 200 205

Asn Glu Ser Pro Trp Arg Ser Asp Leu Leu Ile Asp Glu Asn Cys Leu
210 215 220

Leu Ser Pro Leu Ala Gly Glu Asp Asp Ser Phe Leu Leu Glu Gly Asn
225 230 235 240

Ser Asn Glu Asp Cys Lys Pro Leu Ile Leu Pro Asp Thr Lys Pro Lys
245 250 255

Ile Lys Asp Asn Gly Asp Leu Val Leu Ser Ser Pro Ser Asn Val Thr
260 265 270

Leu Pro Gln Val Lys Thr Glu Lys Glu Asp Phe Ile Glu Leu Cys Thr
275 280 285

Pro Gly Val Ile Lys Gln Glu Lys Leu Gly Thr Val Tyr Cys Gln Ala
290 295 300

Ser Phe Pro Gly Ala Asn Ile Ile Gly Asn Lys Met Ser Ala Ile Ser
305 310 315 320

Val His Gly Val Ser Thr Ser Gly Gly Gln Met Tyr His Tyr Asp Met
325 330 335

Asn Thr Ala Ser Leu Ser Gln Gln Asp Gln Lys Pro Ile Phe Asn
340 345 350

Val Ile Pro Pro Ile Pro Val Gly Ser Glu Asn Trp Asn Arg Cys Gln
355 360 365

Gly Ser Gly Asp Asp Asn Leu Thr Ser Leu Gly Thr Leu Asn Phe Pro
370 375 380

Gly Arg Thr Val Phe Ser Asn Gly Tyr Ser Ser Pro Ser Met Arg Pro
385 390 395 400

Asp Val Ser Ser Pro Pro Ser Ser Ser Thr Ala Thr Thr Gly Pro
405 410 415

Pro Pro Lys Leu Cys Leu Val Cys Ser Asp Glu Ala Ser Gly Cys His
420 425 430

Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys Arg Ala
435 440 445

Val Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp Cys Ile
450 455 460

Ile Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Tyr Arg Lys
465 470 475 480

Cys Leu Gln Ala Gly Met Asn Leu Glu Ala Arg Lys Thr Lys Lys Lys
485 490 495

Ile Lys Gly Ile Gln Gln Ala Thr Thr Gly Val Ser Gln Glu Thr Ser
500 505 510

Glu Asn Pro Gly Asn Lys Thr Ile Val Pro Ala Thr Leu Pro Gln Leu
515 520 525

Thr Pro Thr Leu Val Ser Leu Leu Glu Val Ile Glu Pro Glu Val Leu
530 535 540

Tyr Ala Gly Tyr Asp Ser Ser Val Pro Asp Ser Thr Trp Arg Ile Met
545 550 555 560

Thr Thr Leu Asn Met Leu Gly Gly Arg Gln Val Ile Ala Ala Val Lys
565 570 575

Trp Ala Lys Ala Ile Pro Gly Phe Arg Asn Leu His Leu Asp Asp Gln
580 585 590

Met Thr Leu Leu Gln Tyr Ser Trp Met Phe Leu Met Ala Phe Ala Leu
595 600 605

Gly Trp Arg Ser Tyr Arg Gln Ser Ser Ala Asn Leu Leu Cys Phe Ala
610 615 620

Pro Asp Leu Ile Ile Asn Glu Gln Arg Met Thr Leu Pro Cys Met Tyr
625 630 635 640

Asp Gln Cys Lys His Met Leu Tyr Val Ser Ser Glu Leu His Arg Leu
645 650 655

Gln Val Ser Tyr Glu Glu Tyr Leu Cys Met Lys Thr Leu Leu Leu
660 665 670

Ser Ser Val Pro Lys Asp Gly Leu Lys Ser Gln Glu Leu Phe Asp Glu
675 680 685

Ile Arg Met Thr Tyr Ile Lys Glu Leu Gly Lys Ala Ile Val Lys Arg
690 695 700

Glu Gly Asn Ser Ser Gln Asn Trp Gln Arg Phe Tyr Gln Leu Thr Lys
705 710 715 720

Leu Leu Asp Ser Met His Glu Val Val Glu Asn Leu Leu Asn Tyr Cys
725 730 735

Phe Gln Thr Phe Leu Asp Lys Thr Met Ser Ile Glu Phe Pro Glu Met
740 745 750

Leu Ala Glu Ile Ile Thr Asn Gln Ile Pro Lys Tyr Ser Asn Gly Asn
755 760 765

Ile Lys Lys Leu Leu Phe His Gln Lys
770 775

<210> 14
<211> 933
<212> PRT
<213> Homo sapiens

<220>
<221> DOMAIN
<222> (659)..(918)
<223> minimal ligand binding domain

<400> 14

Met Thr Glu Leu Lys Ala Lys Gly Pro Arg Ala Pro His Val Ala Gly
1 5 10 15

Gly Pro Pro Ser Pro Glu Val Gly Ser Pro Leu Leu Cys Arg Pro Ala
20 25 30

Ala Gly Pro Phe Pro Gly Ser Gln Thr Ser Asp Thr Leu Pro Glu Val
35 40 45

Ser Ala Ile Pro Ile Ser Leu Asp Gly Leu Leu Phe Pro Arg Pro Cys
50 55 60

Gln Gly Gln Asp Pro Ser Asp Glu Lys Thr Gln Asp Gln Gln Ser Leu
65 70 75 80

Ser Asp Val Glu Gly Ala Tyr Ser Arg Ala Glu Ala Thr Arg Gly Ala
85 90 95

Gly Gly Ser Ser Ser Pro Pro Glu Lys Asp Ser Gly Leu Leu Asp
100 105 110

Ser Val Leu Asp Thr Leu Leu Ala Pro Ser Gly Pro Gly Gln Ser Gln
115 120 125

Pro Ser Pro Pro Ala Cys Glu Val Thr Ser Ser Trp Cys Leu Phe Gly
130 135 140

Pro Glu Leu Pro Glu Asp Pro Pro Ala Ala Pro Ala Thr Gln Arg Val
145 150 155 160

Leu Ser Pro Leu Met Ser Arg Ser Gly Cys Lys Val Gly Asp Ser Ser
165 170 175

Gly Thr Ala Ala Ala His Lys Val Leu Pro Arg Gly Leu Ser Pro Ala
180 185 190

Arg Gln Leu Leu Leu Pro Ala Ser Glu Ser Pro His Trp Ser Gly Ala
195 200 205

Pro Val Lys Pro Ser Pro Gln Ala Ala Ala Val Glu Val Glu Glu Glu
210 215 220

Asp Ser Ser Glu Ser Glu Glu Ser Ala Gly Pro Leu Leu Lys Gly Lys
225 230 235 240

Pro Arg Ala Leu Gly Gly Ala Ala Ala Gly Gly Ala Ala Ala Cys
245 250 255

Pro Pro Gly Ala Ala Ala Gly Gly Val Ala Leu Val Pro Lys Glu Asp
260 265 270

Ser Arg Phe Ser Ala Pro Arg Val Ala Leu Val Glu Gln Asp Ala Pro
275 280 285

Met Ala Pro Gly Arg Ser Pro Leu Ala Thr Thr Val Met Asp Phe Ile
290 295 300

His Val Pro Ile Leu Pro Leu Asn His Ala Leu Leu Ala Ala Arg Thr
305 310 315 320

Arg Gln Leu Leu Glu Asp Glu Ser Tyr Asp Gly Gly Ala Gly Ala Ala
325 330 335

Ser Ala Phe Ala Pro Pro Arg Thr Ser Pro Cys Ala Ser Ser Thr Pro
340 345 350

Val Ala Val Gly Asp Phe Pro Asp Cys Ala Tyr Pro Pro Asp Ala Glu
355 360 365

Pro Lys Asp Asp Ala Tyr Pro Leu Tyr Ser Asp Phe Gln Pro Pro Ala
370 375 380

Leu Lys Ile Lys Glu Glu Glu Gly Ala Glu Ala Ser Ala Arg Ser
385 390 395 400

Pro Arg Ser Tyr Leu Val Ala Gly Ala Asn Pro Ala Ala Phe Pro Asp
405 410 415

Phe Pro Leu Gly Pro Pro Pro Leu Pro Pro Arg Ala Thr Pro Ser
420 425 430

Arg Pro Gly Glu Ala Ala Val Thr Ala Ala Pro Ala Ser Ala Ser Val
435 440 445

Ser Ser Ala Ser Ser Gly Ser Thr Leu Glu Cys Ile Leu Tyr Lys
450 455 460

Ala Glu Gly Ala Pro Pro Gln Gln Gly Pro Phe Ala Pro Pro Pro Cys
465 470 475 480

Lys Ala Pro Gly Ala Ser Gly Cys Leu Leu Pro Arg Asp Gly Leu Pro
485 490 495

Ser Thr Ser Ala Ser Ala Ala Ala Gly Ala Ala Pro Ala Leu Tyr
500 505 510

Pro Ala Leu Gly Leu Asn Gly Leu Pro Gln Leu Gly Tyr Gln Ala Ala
515 520 525

Val Leu Lys Glu Gly Leu Pro Gln Val Tyr Pro Pro Tyr Leu Asn Tyr
530 535 540

Leu Arg Pro Asp Ser Glu Ala Ser Gln Ser Pro Gln Tyr Ser Phe Glu
545 550 555 560

Ser Leu Pro Gln Lys Ile Cys Leu Ile Cys Gly Asp Glu Ala Ser Gly
565 570 575

Cys His Tyr Gly Val Leu Thr Cys Gly Ser Cys Lys Val Phe Phe Lys
580 585 590

Arg Ala Met Glu Gly Gln His Asn Tyr Leu Cys Ala Gly Arg Asn Asp
595 600 605

Cys Ile Val Asp Lys Ile Arg Arg Lys Asn Cys Pro Ala Cys Arg Leu
610 615 620

Arg Lys Cys Cys Gln Ala Gly Met Val Leu Gly Gly Arg Lys Phe Lys
625 630 635 640

Lys Phe Asn Lys Val Arg Val Val Arg Ala Leu Asp Ala Val Ala Leu
645 650 655

Pro Gln Pro Leu Gly Val Pro Asn Glu Ser Gln Ala Leu Ser Gln Arg
660 665 670

Phe Thr Phe Ser Pro Gly Gln Asp Ile Gln Leu Ile Pro Pro Leu Ile
675 680 685

Asn Leu Leu Met Ser Ile Glu Pro Asp Val Ile Tyr Ala Gly His Asp
690 695 700

Asn Thr Lys Pro Asp Thr Ser Ser Ser Leu Leu Thr Ser Leu Asn Gln
705 710 715 720

Leu Gly Glu Arg Gln Leu Leu Ser Val Val Lys Trp Ser Lys Ser Leu
725 730 735

Pro Gly Phe Arg Asn Leu His Ile Asp Asp Gln Ile Thr Leu Ile Gln
740 745 750

Tyr Ser Trp Met Ser Leu Met Val Phe Gly Leu Gly Trp Arg Ser Tyr
755 760 765

Lys His Val Ser Gly Gln Met Leu Tyr Phe Ala Pro Asp Leu Ile Leu
770 775 780

Asn Glu Gln Arg Met Lys Glu Ser Ser Phe Tyr Ser Leu Cys Leu Thr
785 790 795 800

Met Trp Gln Ile Pro Gln Glu Phe Val Lys Leu Gln Val Ser Gln Glu
805 810 815

Glu Phe Leu Cys Met Lys Val Leu Leu Leu Asn Thr Ile Pro Leu
820 825 830

Glu Gly Leu Arg Ser Gln Thr Gln Phe Glu Glu Met Arg Ser Ser Tyr
835 840 845

Ile Arg Glu Leu Ile Lys Ala Ile Gly Leu Arg Gln Lys Gly Val Val
850 855 860

Ser Ser Ser Gln Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Asn Leu
865 870 875 880

His Asp Leu Val Lys Gln Leu His Leu Tyr Cys Leu Asn Thr Phe Ile
885 890 895

Gln Ser Arg Ala Leu Ser Val Glu Phe Pro Glu Met Met Ser Glu Val
900 905 910

Ile Ala Ala Gln Leu Pro Lys Ile Leu Ala Gly Met Val Lys Pro Leu
915 920 925

Leu Phe His Lys Lys
930

<210> 15
<211> 984
<212> PRT
<213> Homo sapiens

<220>
<221> DOMAIN
<222> (695)..(969)
<223> minimal ligand binding domain

<400> 15

Met Glu Thr Lys Gly Tyr His Ser Leu Pro Glu Gly Leu Asp Met Glu
1 5 10 15

Arg Arg Trp Gly Gln Val Ser Gln Ala Val Glu Arg Ser Ser Leu Gly
20 25 30

Pro Thr Glu Arg Thr Asp Glu Asn Asn Tyr Met Glu Ile Val Asn Val

35

40

45

Ser Cys Val Ser Gly Ala Ile Pro Asn Asn Ser Thr Gln Gly Ser Ser
 50 55 60

Lys Glu Lys Gln Glu Leu Leu Pro Cys Leu Gln Gln Asp Asn Asn Arg
 65 70 75 80

Pro Gly Ile Leu Thr Ser Asp Ile Lys Thr Glu Leu Glu Ser Lys Glu
 85 90 95

Leu Ser Ala Thr Val Ala Glu Ser Met Gly Leu Tyr Met Asp Ser Val
 100 105 110

Arg Asp Ala Asp Tyr Ser Tyr Glu Gln Gln Asn Gln Gly Ser Met
 115 120 125

Ser Pro Ala Lys Ile Tyr Gln Asn Val Glu Gln Leu Val Lys Phe Tyr
 130 135 140

Lys Gly Asn Gly His Arg Pro Ser Thr Leu Ser Cys Val Asn Thr Pro
 145 150 155 160

Leu Arg Ser Phe Met Ser Asp Ser Gly Ser Ser Val Asn Gly Gly Val
 165 170 175

Met Arg Ala Ile Val Lys Ser Pro Ile Met Cys His Glu Lys Ser Pro
 180 185 190

Ser Val Cys Ser Pro Leu Asn Met Thr Ser Ser Val Cys Ser Pro Ala
 195 200 205

Gly Ile Asn Ser Val Ser Ser Thr Thr Ala Ser Phe Gly Ser Phe Pro
 210 215 220

Val His Ser Pro Ile Thr Gln Gly Thr Pro Leu Thr Cys Ser Pro Asn
 225 230 235 240

Ala Glu Asn Arg Gly Ser Arg Ser His Ser Pro Ala His Ala Ser Asn
 245 250 255

Val Gly Ser Pro Leu Ser Ser Pro Leu Ser Ser Met Lys Ser Ser Ile
 260 265 270

Ser Ser Pro Pro Ser His Cys Ser Val Lys Ser Pro Val Ser Ser Pro
 275 280 285

Asn Asn Val Thr Leu Arg Ser Ser Val Ser Ser Pro Ala Asn Ile Asn
 290 295 300

Asn Ser Arg Cys Ser Val Ser Ser Pro Ser Asn Thr Asn Asn Arg Ser
 305 310 315 320

Thr Leu Ser Ser Pro Ala Ala Ser Thr Val Gly Ser Ile Cys Ser Pro
 325 330 335

Val Asn Asn Ala Phe Ser Tyr Thr Ala Ser Gly Thr Ser Ala Gly Ser

340

345

350

Ser Thr Leu Arg Asp Val Val Pro Ser Pro Asp Thr Gln Glu Lys Gly
355 360 365

Ala Gln Glu Val Pro Phe Pro Lys Thr Glu Glu Val Glu Ser Ala Ile
370 375 380

Ser Asn Gly Val Thr Gly Gln Leu Asn Ile Val Gln Tyr Ile Lys Pro
385 390 395 400

Glu Pro Asp Gly Ala Phe Ser Ser Ser Cys Leu Gly Gly Asn Ser Lys
405 410 415

Ile Asn Ser Asp Ser Ser Phe Ser Val Pro Ile Lys Gln Glu Ser Thr
420 425 430

Lys His Ser Cys Ser Gly Thr Ser Phe Lys Gly Asn Pro Thr Val Asn
435 440 445

Pro Phe Pro Phe Met Asp Gly Ser Tyr Phe Ser Phe Met Asp Asp Lys
450 455 460

Asp Tyr Tyr Ser Leu Ser Gly Ile Leu Gly Pro Pro Val Pro Gly Phe
465 470 475 480

Asp Gly Asn Cys Glu Gly Ser Gly Phe Pro Val Gly Ile Lys Gln Glu
485 490 495

Pro Asp Asp Gly Ser Tyr Tyr Pro Glu Ala Ser Ile Pro Ser Ser Ala
500 505 510

Ile Val Gly Val Asn Ser Gly Gly Gln Ser Phe His Tyr Arg Ile Gly
515 520 525

Ala Gln Gly Thr Ile Ser Leu Ser Arg Ser Ala Arg Asp Gln Ser Phe
530 535 540

Gln His Leu Ser Ser Phe Pro Pro Val Asn Thr Leu Val Glu Ser Trp
545 550 555 560

Lys Ser His Gly Asp Leu Ser Ser Arg Arg Ser Asp Gly Tyr Pro Val
565 570 575

Leu Glu Tyr Ile Pro Glu Asn Val Ser Ser Ser Thr Leu Arg Ser Val
580 585 590

Ser Thr Gly Ser Ser Arg Pro Ser Lys Ile Cys Leu Val Cys Gly Asp
595 600 605

Glu Ala Ser Gly Cys His Tyr Gly Val Val Thr Cys Gly Ser Cys Lys
610 615 620

Val Phe Phe Lys Arg Ala Val Glu Gly Gln His Asn Tyr Leu Cys Ala
625 630 635 640

Gly Arg Asn Asp Cys Ile Ile Asp Lys Ile Arg Arg Lys Asn Cys Pro

645 650 655

Ala Cys Arg Leu Gln Lys Cys Leu Gln Ala Gly Met Asn Leu Gly Ala
660 665 670

Arg Lys Ser Lys Lys Leu Gly Lys Leu Lys Gly Ile His Glu Glu Gln
675 680 685

Pro Gln Gln Gln Gln Pro Pro Pro Pro Pro Pro Pro Gln Ser Pro
690 695 700

Glu Glu Gly Thr Thr Tyr Ile Ala Pro Ala Lys Glu Pro Ser Val Asn
705 710 715 720

Thr Ala Leu Val Pro Gln Leu Ser Thr Ile Ser Arg Ala Leu Thr Pro
725 730 735

Ser Pro Val Met Val Leu Glu Asn Ile Glu Pro Glu Ile Val Tyr Ala
740 745 750

Gly Tyr Asp Ser Ser Lys Pro Asp Thr Ala Glu Asn Leu Leu Ser Thr
755 760 765

Leu Asn Arg Leu Ala Gly Lys Gln Met Ile Gln Val Val Lys Trp Ala
770 775 780

Lys Val Leu Pro Gly Phe Lys Asn Leu Pro Leu Glu Asp Gln Ile Thr
785 790 795 800

Leu Ile Gln Tyr Ser Trp Met Cys Leu Ser Ser Phe Ala Leu Ser Trp
805 810 815

Arg Ser Tyr Lys His Thr Asn Ser Gln Phe Leu Tyr Phe Ala Pro Asp
820 825 830

Leu Val Phe Asn Glu Glu Lys Met His Gln Ser Ala Met Tyr Glu Leu
835 840 845

Cys Gln Gly Met His Gln Ile Ser Leu Gln Phe Val Arg Leu Gln Leu
850 855 860

Thr Phe Glu Glu Tyr Thr Ile Met Lys Val Leu Leu Leu Leu Ser Thr
865 870 875 880

Ile Pro Lys Asp Gly Leu Lys Ser Gln Ala Ala Phe Glu Glu Met Arg
885 890 895

Thr Asn Tyr Ile Lys Glu Leu Arg Lys Met Val Thr Lys Cys Pro Asn
900 905 910

Asn Ser Gly Gln Ser Trp Gln Arg Phe Tyr Gln Leu Thr Lys Leu Leu
915 920 925

Asp Ser Met His Asp Leu Val Ser Asp Leu Leu Glu Phe Cys Phe Tyr
930 935 940

Thr Phe Arg Glu Ser His Ala Leu Lys Val Glu Phe Pro Ala Met Leu

945 950 955 960

Val Glu Ile Ile Ser Asp Gln Leu Pro Lys Val Glu Ser Gly Asn Ala
965 970 975

Lys Pro Leu Tyr Phe His Arg Lys
980

<210> 16
<211> 452
<212> PRT
<213> Homo sapiens

<220>
<221> DOMAIN
<222> (184)..(437)
<223> minimal ligand binding domain

<400> 16

Gly Gly Gly Gly Gly Glu Ala Gly Ala Val Ala Pro Tyr Gly Tyr Thr
1 5 10 15

Arg Pro Pro Gln Gly Leu Ala Gly Gln Glu Ser Asp Phe Thr Ala Pro
20 25 30

Asp Val Trp Tyr Pro Gly Gly Met Val Ser Arg Val Pro Tyr Pro Ser
35 40 45

Pro Thr Cys Val Lys Ser Glu Met Gly Pro Trp Met Asp Ser Tyr Ser
50 55 60

Gly Pro Tyr Gly Asp Met Arg Leu Glu Thr Ala Arg Asp His Val Leu
65 70 75 80

Pro Ile Asp Tyr Tyr Phe Pro Pro Gln Lys Thr Cys Leu Ile Cys Gly
85 90 95

Asp Lys Ala Ser Gly Cys His Tyr Gly Ala Leu Thr Cys Gly Ser Cys
100 105 110

Lys Val Phe Phe Lys Arg Ala Ala Glu Gly Lys Gln Lys Tyr Leu Cys
115 120 125

Ala Ser Arg Asn Asp Cys Thr Ile Asp Lys Phe Arg Arg Lys Asn Cys
130 135 140

Pro Ser Cys Arg Leu Arg Lys Cys Tyr Glu Ala Gly Met Thr Leu Gly
145 150 155 160

Ala Arg Lys Leu Lys Lys Leu Gly Asn Leu Lys Leu Gln Glu Glu Gly
165 170 175

Glu Ala Ser Ser Thr Thr Ser Pro Thr Glu Glu Thr Thr Gln Lys Leu
180 185 190

Thr Val Ser His Ile Glu Gly Tyr Glu Cys Gln Pro Ile Phe Leu Asn
195 200 205

Val Leu Glu Ala Ile Glu Pro Gly Val Val Cys Ala Gly His Asp Asn
210 215 220

Asn Gln Pro Asp Ser Phe Ala Ala Leu Leu Ser Ser Leu Asn Glu Leu
225 230 235 240

Gly Glu Arg Gln Leu Val His Val Val Lys Trp Ala Lys Ala Leu Pro
245 250 255

Gly Phe Arg Asn Leu His Val Asp Asp Gln Met Ala Val Ile Gln Tyr
260 265 270

Ser Trp Met Gly Leu Met Val Phe Ala Met Gly Trp Arg Ser Phe Thr
275 280 285

Asn Val Asn Ser Arg Met Leu Tyr Phe Ala Pro Asp Leu Val Phe Asn
290 295 300

Glu Tyr Arg Met His Lys Ser Arg Met Tyr Ser Gln Cys Val Arg Met
305 310 315 320

Arg His Leu Ser Gln Glu Phe Gly Trp Leu Gln Ile Thr Pro Gln Glu
325 330 335

Phe Leu Cys Met Lys Ala Leu Leu Phe Ser Ile Ile Pro Val Asp
340 345 350

Gly Leu Lys Asn Gln Lys Phe Phe Asp Glu Leu Arg Met Asn Tyr Ile
355 360 365

Lys Glu Leu Asp Arg Ile Ile Ala Cys Lys Arg Lys Asn Pro Thr Ser
370 375 380

Cys Ser Arg Arg Phe Tyr Gln Leu Thr Lys Leu Leu Asp Ser Val Gln
385 390 395 400

Pro Ile Ala Arg Glu Leu His Gln Phe Thr Phe Asp Leu Leu Ile Lys
405 410 415

Ser His Met Val Ser Val Asp Phe Pro Glu Met Met Ala Glu Ile Ile
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Ser Val Gln Val Pro Lys Ile Leu Ser Gly Lys Val Lys Pro Ile Tyr
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Phe His Thr Gln
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16